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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/993,234	11/19/2001	Avi J. Ashkenazi	P1007P1DI	1337
9157	7590	10/07/2003	EXAMINER	
GENENTECH, INC. 1 DNA WAY SOUTH SAN FRANCISCO, CA 94080			NICKOL, GARY B	
			ART UNIT	PAPER NUMBER
			1642	
DATE MAILED: 10/07/2003				

10

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/993,234	ASHKENAZI, AVI J.	
	Examiner	Art Unit	
	Gary B. Nickol Ph.D.	1642	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1) Responsive to communication(s) filed on 17 July 2003.

2a) This action is FINAL. 2b) This action is non-final.

3) Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4) Claim(s) 34-39 and 46-94 is/are pending in the application.

4a) Of the above claim(s) 35 and 46-94 is/are withdrawn from consideration.

5) Claim(s) _____ is/are allowed.

6) Claim(s) 34 and 36-39 is/are rejected.

7) Claim(s) _____ is/are objected to.

8) Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9) The specification is objected to by the Examiner.

10) The drawing(s) filed on _____ is/are: a) accepted or b) objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11) The proposed drawing correction filed on _____ is: a) approved b) disapproved by the Examiner.
If approved, corrected drawings are required in reply to this Office action.

12) The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

13) Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a) All b) Some * c) None of:

1. Certified copies of the priority documents have been received.
2. Certified copies of the priority documents have been received in Application No. _____.
3. Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14) Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).

a) The translation of the foreign language provisional application has been received.

15) Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892)	4) <input type="checkbox"/> Interview Summary (PTO-413) Paper No(s). _____.
2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948)	5) <input type="checkbox"/> Notice of Informal Patent Application (PTO-152)
3) <input checked="" type="checkbox"/> Information Disclosure Statement(s) (PTO-1449) Paper No(s) <u>5</u> .	6) <input type="checkbox"/> Other: _____.

DETAILED ACTION

The response filed on July 17, 2003 (Paper No. 9) to the restriction requirement of March 26, 2003 has been received. Applicant has elected the species corresponding to nucleic acids encoding amino acids 25-198 of SEQ ID NO:6. Because applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (MPEP 818.03(a)).

Claims 34-39, and 46-94 are pending.

Claims 35, 46-94 are withdrawn from further consideration by the examiner under 37 CFR 1.142(b), as being drawn to a non-elected invention. (It is noted that applicant believes that pending claims 34, 36-39, and 91-94 are readable on the elected invention—see Paper No. 9, page 2. However, nowhere do claims 91-94 recite nucleic acids encoding amino acids 25-198. Thus, claims 91-94 are withdrawn from consideration.)

Claims 34, and 36-39 are pending and are currently under examination.

Priority

A review of the parent applications (08/828,683; 08/625,328; 08/710,802) revealed priority to application No. 08/710,802 filed 09/23/1996. If applicant disagrees with any rejection of claims 34, 36-39 set forth in this office action based on examiner's establishment of a priority date of **September 23, 1996** for the instant claims in application serial number 09/993,234, applicant is invited to submit evidence pointing to the serial number, page and line where support can be found establishing an earlier priority date.

Information Disclosure Statement

References 210-233, and 235 are improperly cited and will not be printed for publication because they lack publication dates. See 37 CFR 1.98 (b) (5).

Specification

The attempt to update the priority status of the present application as set forth in the preliminary amendment of Paper No. 6 is incomplete. Applicants should indicate that U.S. Serial no. 08/828,683 filed March 31, 1997 is now U.S. Patent No. 6,469,144.

The description of the figures on page 11 (in particular Figures 1-2, 3, 5-6) in which sequences are referenced is incomplete for improper disclosure of amino acid sequences without inclusion of a sequence identifier (i.e., SEQ ID NO:). Thus, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825. This definition sets forth limits, in terms of numbers of amino acids and/or numbers of nucleotides, at or above which compliance with the sequence rules is required. Amino acid sequences as used in 37 CFR 1.821 through 1.825 are interpreted to mean an unbranched sequence of four or more amino acids.

Thus, applicant should amend the specification to insert the appropriate sequence identifier of each referred to sequence. If these sequences have *not* been previously disclosed in a CRF, applicant must provide a computer readable form (CRF) of the sequence listing, an initial or substitute paper copy of the sequence listing, as well as any amendment directing its entry into the specification, and a statement that the content of the paper and computer readable

copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e-f) or 1.825(b) or 1.825(d). *Failure to supply the appropriate sequences identification numbers in response to this action will be considered non-responsive.*

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claim 39 is rejected under 35 U.S.C. 112, second paragraph, as being incomplete for omitting essential steps, such omission amounting to a gap between the steps. See MPEP § 2172.01. The claim is drawn to a process of using a nucleic acid molecule encoding Apo-3 to effect production of Apo-3. It is not distinctly clear how using the nucleic acid will “effect production”. Thus, there appears to be a step missing. The rejection can be obviated by amending the claim to a process of producing an Apo-3 polypeptide comprising culturing the host cell of Claim 38 and isolating said polypeptide.

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claim 34 is rejected under 35 USC 112, first paragraph, as the specification does not contain a written description of the claimed invention. The limitation of isolated nucleic acid

encoding Apo-3 polypeptide comprising amino acid residues **25-417** has no clear support in the specification and the claims as originally filed. Hence, this is a new matter rejection. Applicant should cancel this terminology or submit evidence pointing to the serial number, page and line where support can be found for the disputed terminology.

Claims 34, and 36-39 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The written description in this case only sets forth an isolated nucleic acid encoding Apo-3 polypeptide comprising amino acid residues 1 to 417, 25 to 198, or 338 to 417 of SEQ ID NO:6. Therefore the written description is not commensurate in scope with the claims inclusive of isolated nucleic acids encoding “a biologically active variant thereof”.

To provide adequate written description and evidence of possession of a claimed genus, the specification must provide sufficient distinguishing identifying characteristics of the genus. The factors to be considered include disclosure of complete or partial structure, physical and/or chemical properties, functional characteristics, structure/function correlation, methods of making the claimed product, or any combination thereof. In this case, no such factors are attributed to the claimed variant. Further, there is no identification of any particular portion of the variant that must be conserved. Accordingly, in the absence of sufficient recitation of distinguishing identifying characteristics, the specification does not provide adequate written description of the claimed genus.

Vas-Cath Inc. v. Mahurkar, 19 USPQ2d 1111, clearly states “applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of the invention. The invention is, for purposes of the ‘written description’ inquiry, whatever is now claimed.” (See page 1117.) The specification does not “clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed.” (See *Vas-Cath* at page 1116). As discussed above, the skilled artisan cannot envision the detailed chemical structure of nucleic acids encoding the encompassed genus of variant polypeptides, and therefore conception is not achieved until reduction to practice has occurred, regardless of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method of isolating it. The compound itself is required. See *Fiers v. Revel*, 25 USPQ2d 1601 at 1606 (CAFC 1993) and *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ2d 1016.

One cannot describe what one has not conceived. See *Fiddes v. Baird*, 30 USPQ2d 1481 at 1483. In *Fiddes*, claims directed to mammalian FGF's were found to be unpatentable due to lack of written description for that broad class. The specification provided only the bovine sequence.

Therefore, only isolated nucleic acid encoding Apo-3 polypeptide comprising amino acid residues 1 to 417, 25 to 198, or 338 to 417 of SEQ ID NO:6, but not the full breadth of the claim meets the written description provision of 35 U.S.C. §112, first paragraph. Applicant is reminded that *Vas-Cath* makes clear that the written description provision of 35 U.S.C. §112 is severable from its enablement provision (see page 1115).

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

Claims 34, 36-39 are rejected under 35 U.S.C. 102(e) as being anticipated by Yu *et al.* (US Patent No. 6,153,402; *earliest priority date is March 12, 1996*; IDS #25 and #26).

Yu *et al.* teach an isolated nucleic acid encoding amino acid residues 25-198 (see attached sequence comparison; also see page 67 of US Provisional 60/013,285 beginning at amino acid position No. 36). Yu *et al.* further teach vectors, host cells, and a process of using said host cells to effect production of the polypeptide comprising culturing the host cell (page 5, 2nd paragraph, of 60/013,285).

Claims 34, and 36-39 are also rejected under 35 U.S.C. 102(e) as being anticipated by Feldmann *et al.* (US Patent No. 5633145; *earliest priority date is May 30, 1993*)

Feldmann *et al.* teach an isolated nucleic acid encoding a biologically active variant polypeptide. (see attached sequence comparison; isolated DNA encoding the variant polypeptide is 39% similar to SEQ ID NO:6). Feldmann *et al.* further teach recombinant expression of biologically active variant polypeptides via host cells transfected with vectors (column 5).

No claim is allowed.

Art Unit: 1642

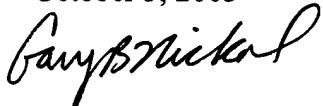
Any inquiry concerning this communication or earlier communications from the examiner should be directed to Gary B. Nickol Ph.D. whose telephone number is 703-305-7143. The examiner can normally be reached on M-F, 8:30-5:00 P.M..

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Anthony Caputa can be reached on 703-308-3995. The fax phone numbers for the organization where this application or proceeding is assigned are 703-305-3014 for regular communications and 703-308-4242 for After Final communications.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is 703-308-0196.

Gary B. Nickol, Ph.D.
Examiner
Art Unit 1642

GBN
October 3, 2003



ATTORNEY/AGENT INFORMATION:	
NAME: Steffe, Eric K.	
REGISTRATION NUMBER: 36,688	
REFERENCE/DOCKET NUMBER: 1488-031003/EKS/KRM	
TELECOMMUNICATION INFORMATION:	
TELEPHONE: 202-371-2540	
FAX: 202-371-2600	
INFORMATION FOR SEQ ID NO: 3:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 1254 base pairs	
STRANDEDNESS: double	
TOPOLogy: nucleic acid	
MOLECULE TYPE: cDNA	
FEATURE: NAME/KEY: CDS	
LOCATION: 1..1251	
PRIORITY: 08-815-469-3	
COMMENT Scores:	
. No.: 3.22e-86	
. re: 1038.00	
. cent Similarity: 100.00%	
. Local Similarity: 100.00%	
. Feature Match: 100.00%	
Length: 1254	
Matches: 174	
Conservative: 0	
Mismatches: 0	
Indels: 0	
Gaps: 0	
1 GlnglyglylhrarSerProargcysAspcysAlaGlyAsphehistlysilegyl 20	
73 CAGGGCGCACTCGTACGCCAGGTGACTGTCGGGAGACTTCACAAAGAGATGGT 132	
21 LeupheCysCysArglycysproAlaGlyHistyleuLysAlaProCysThrGluPro 40	
133 CTGTTTGTTGAGAGCCGCTGCTGAGCCCTGATGAGCCCTGGAGCCC 192	
41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuLysAlaProCys 60	
193 TGGGCCACTCCACCTGCTTGTGTCGCCAGAACCTCTTGCCCTGGAGAACAC 252	
61 HisAsnSerGluCysAlaArgGlyGlnAlaSerGluGlnAlaSerGlnAlaLeu 80	
253 CATAATCTGAATGTCGCCGCGCAGGCCAGCTGATGAGCCCTGGAGCCC 312	
81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100	
313 GGAACGCTTCAGCCAAATGTCAGCACTTCACCTCTACTCCAACTCATGCCTAGTC 432	
121 GlyAlaLeuHisArgIleLysSerAlaArgGlyAspThrSerThrLeu 140	
433 GGGGCCTGCAACGCCACACAGGCTACTCTGTCGGCAGAGATACTGAGGGACC 492	
141 CysLeuProGlyPheTyrglyLysGlyCysValSerCysProThrSerThrLeu 160	
493 TGGCCTGCCGCTCTGATGACATGCGGATGCGCTGCTGCCAGAGACCTCTGGAGG 552	
DUT 2	
08-928-069-11	
Sequence 11, Application US/08928069	
Attent. No. 6462176	
GENERAL INFORMATION:	
APPLICANT: Ashkenazi, Avi J.	
TITLE OF INVENTION: Apo-3 polypeptide	
NUMBER OF SEQUENCES: 15	
CORRESPONDENCE ADDRESS:	
ADDRESSEE: Genentech, Inc.	
STREET: 1 DNA Way	
CITY: South San Francisco	
STATE: California	
COUNTRY: USA	
ZIP: 94060	
COMPUTER READABLE FORM:	
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk	
COMPUTER: IBM PC compatible	
OPERATING SYSTEM: PC-DOS/MS-DOS	
SOFTWARE: WinPatin (Genentech)	
CURRENT APPLICATION DATA:	
APPLICATION NUMBER: US/08/928, 069	
FILING DATE: 11-Sep-1997	
CLASSIFICATION: 435	
PRIOR APPLICATION DATA:	
APPLICATION NUMBER: 60/026943	
FILING DATE: 09/23/1996	
ATTORNEY/AGENT INFORMATION:	
NAME: Marschang, Diane L.	
REGISTRATION NUMBER: 35,600	
REFERENCE/DOCKET NUMBER: P1052R1	
TELECOMMUNICATION INFORMATION:	
TELEPHONE: 650/225-5416	
TELEFAX: 650/952-9881	
INFORMATION FOR SEQ ID NO: 11:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 1634 base pairs	
TYPE: Nucleic Acid	
STRANDEDNESS: Single	
TOPOLogy: Linear	
US-08-928-069-11	
Alignment Scores:	
. Pred. No.: 4.57e-86	
. Score: 1038.00	
. Percent Similarity: 100.00%	
. Best Local Similarity: 100.00%	
. Query Match: 100.00%	
DB: 4	
DB: Gaps: 0	
US-09-993-234-6_COPY_25_198 (1-174) x US-08-928-069-11 (1-1634)	
Qy 1 GlnglyglylhrarSerProargcysAspcysAlaGlyAsphehistlysilegyl 20	
Db 161 CAGGGCGCACTCGTACGCCAGGGCTACTCTGAGGCCCTTCACGGAGCC 280	
Qy 41 CysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaProCys 60	
Db 281 TGGCCTGCCGCTCTGATGACATGCGGATGCGCTGCCAGAGACCTCTGGAGG 340	
Qy 61 HisAsnSerGluCysAlaArgGlyGlnAlaCysAspGluGlnAlaSerGlnAlaLeu 80	
Db 341 CATAATCTGAATGTCGCCAGCCGCTGCGCTGCTGCCAGAGACCTCTGGAGG 400	
Qy 81 GluAsnCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyTrpPheValGlu 100	
Db 401 GAGACTGTCAGCACTGCTGAGCTGCTGAGCTGCTGAGCTGCTGAGCTGCTGAGCTG 460	
Qy 101 CysGlyValSerGlyCysValSerSerSerProPheCysGlnProCysLeuAspys 120	
Db 461 TCCGAGTCAGCACTGCTGAGCTGCTGAGCTGCTGAGCTGCTGAGCTGAGCTG 520	
Qy 121 GlyAlaLeuHisArgIleLysSerAlaArgLeuCysSerArgAspThrAspCysGlyThr 140	
Db 521 GGGCCTGCCGCTCTGATGACATGCGGATGCGCTGCCAGAGACCTCTGGAGG 580	

US-09-993-234-6 (1-417) x US-08-050-319B-24 (1-2062)

QY 334 GluLeuIysRaspvalmetAspAlaValProIalaArgArgTrpLysGluPheValArgThr 353
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1413 ACCGTGACGGCTGCGGAGCCGCCGTCGCCTGCGCTGAAAGGATGTTGGCGCGG 1472
 QY 354 LeuGlyLeuArgGluLalaGluLalaGluLalaGluLalaGluLalaGluLalaGlyArg--PheArg 372
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1473 CTGGGACTGAGCAGAGATCGAGCAGGCTGGAGAAGGGCCACCTGGCC 1532
 QY 373 AspGlnGlnTrpLysArgTrpArgGlnGlnInPro-----AlaGly 389
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 1533 GAGGCCAGTACAGCATGCTGGCCGCTGGCCGCCAGCCGGCCGAGGCCACG 1592
 QY 390 LeuGlyLalaValtyalaAlaLeuGluArgMetGlyLeuAspGlyCysValGluAspIle 409
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 -Db 1593 CTGGAGCTGCTGGCCGCTGCTCAGGGCACWGAACCTGAGGCTGAGGCTGCTGGAAACATA 1652
 QY 410 ArgSerArgLeu 413
 Db 1653 GAGGAGGCGCTG 1664
 QY 84 HIS-HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnAla 103
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 437 CACCRCAGA---CACGCTGCAGCTGGACGGGACACCTGCTGCTGGTCAGGCTGAG 493
 QY 104 LeuGluAsnCysSerAlaValAlaLeuAspThrArgCysGlyCysLysProGlyPheVal 123
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 494 ATCTCTCTGTCACAGTGACGCTGCTGCTGCAAAAGCAGGAAATATGCCCTCAAAAT 316
 QY 124 GluCys-----GlnValSerGlnCysValSerSerProPheTyrcysGlnInPro 140
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 554 CATATGGCTGAAACCTTTCAGGIC-----TCAATTGAGCC 598
 QY 141 CysteauAspCysGlyValLeuHisArgHisThrArgLeuIeuCysSerTargGasPhe 160
 ||||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 599 TGCCCTCAAT---GGACCGTGCAC-----CTCCTCTGCAAGGAGAACAGAAC 643
 QY 161 AspCysGlyIhrCysLeuProGlyPheTrpGluHisGlyAspGlyCysValSerCysPro 180
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 644 ACCGRTGACCTSCCATGCAAGGTTCTTAAGAGAAAACGAGTGTCTCTCTGT--- 700
 QY 181 ThrSerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys----- 195
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 701 -----AGTAACTGTAAGAAGAACCTGGAGTGGCACGAGTGTGCTAACCCAG 748
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 ||||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 749 ATTGAGGAATGTTAAGGCCTGAGGACTCTGGCCTGCTGCCCCTGCTCATT 808
 QY 207 LeuAlaGlyLeuIeuValProLeuLeuLeuGlyAlaThrLeuThrThrThrArgHis 226
 ||||| ||||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 809 TTCTTGTGTTGTTGCTTATCCCTCTCTCATTTGTTAAATGCTATGCTTACCAAGG 868
 QY 227 CysteProHisLys-----ProLeuValThrAlaAspGluAla 239
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 Db 869 ---TGGAAAGTCCAGCTCTACTCCATGTTGGAAATCGCACCTGAAAGAGGG 925
 QY 240 GlyMetGluAlaLeuThrProProAlaLalaLeuSerProLeuAspSer----- 257
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 926 GAGCTTGAGGACTACTACTAAAGCC-----CTGGCCCAACCCAAGCTTACT 976
 QY 258 -----AlaHistidineLeuAlaProProAspSerSerGluLysileys 272
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 977 CCCACTCCAGGTCACCCACCTGGCTTCAGTCCCCTGCCACCTTACCC 1036
 QY 273 ThrValGlnIeuValThrItpSerTrpGlnLeuProSerArgAlaLeuGlyPro--- 310
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 1064 TGTCCCAACTTGCG-----GCTCCCGAGAGGGTGCACCCCTAT 1108
 QY 311 -----AlaAlaAlaProProLeuSerPro--- 318
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 1109 CACCCGCCACCCGCCACCCGCCACCCGCCACCCGCCACCCGCCACCC 1166
 QY 15 LeuLeuIeuValLeuLeuGlyAlaArgAlaGlyGly----- 26
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 197 CTCCCTGAGCTGTTGGATATAACCCCTCAGGGTTATGGACTGGTCCCCTCACCTA 256
 QY 27 GlyTrpArgSerProArg-----CysAspCysAlaGlyAspPheHisLysSle 43
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 257 GGGGACGSSGAGAGAGATACTGTTGTCGCCAAAGGAAATATTCACCCCTCACCTA 316
 QY 44 GlyLeuPheCysCysArgGlyCysProAlaGlyHistylLeuLysAlaProCysThrGlu 63
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 Db 317 AATTCGATTCGCTGACCAAGTGGCCACAAGAACCTACTTGTCATCTGTCAGGC 376
 QY 64 ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGlu 83
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 377 CGGGCCAGGATACCGACTGCAAGGGTGTGAGAGGCCCTCTCACCCCTCACAAAC 436
 QY 84 HIS-HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnAla 103
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 437 CACCRCAGA---CACGCTGCAGCTGCTGCTGCAAAAGCAGGAAATATGCCCTCACCTA 316
 QY 104 LeuGluAsnCysSerAlaValAlaLeuAspThrArgCysGlyCysLysProGlyPheVal 123
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 Db 494 ATCTCTCTGTCACAGTGACGCTGCTGCTGCAAAAGCAGGAAATATGCCCTCACCTA 316
 QY 124 GluCys-----GlnValSerGlnCysValSerSerProPheTyrcysGlnInPro 140
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 554 CATATGGCTGAAACCTTTCAGGIC-----TCAATTGAGCC 598
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 Db 599 TGCCCTCAAT---GGACCGTGCAC-----CTCCTCTGCAAGGAGAACAGAAC 643
 QY 161 AspCysGlyIhrCysLeuProGlyPheTrpGluHisGlyAspGlyCysValSerCysPro 180
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 644 ACCGRTGACCTSCCATGCAAGGTTCTTAAGAGAAAACGAGTGTCTCTCTGT--- 700
 QY 181 ThrSerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys----- 195
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 701 -----AGTAACTGTAAGAAGAACCTGGAGTGGCACGAGTGTGCTAACCCAG 748
 QY 196 -----GlyTrpArgGlnMetPheTrpArgValGlnVal 206
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 749 ATTGAGGAATGTTAAGGCCTGAGGACTCTGGCCTGCTGCCCCTGCTCATT 808
 QY 207 LeuAlaGlyLeuIeuValProLeuLeuLeuGlyAlaThrLeuThrThrArgHis 226
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 809 TTCTTGTGTTGTTGCTTATCCCTCTCTCATTTGTTAAATGCTATGCTTACCAAGG 868
 QY 227 CysteProHisLys-----ProLeuValThrAlaAspGluAla 239
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 869 ---TGGAAAGTCCAGCTCTACTCCATGTTGGAAATCGCACCTGAAAGAGGG 925
 QY 240 GlyMetGluAlaLeuThrProProAlaLalaLeuSerProLeuAspSer----- 257
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 926 GAGCTTGAGGACTACTACTAAAGCC-----CTGGCCCAACCCAAGCTTACT 976
 QY 258 -----AlaHistidineLeuAlaProProAspSerSerGluLysileys 272
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 977 CCCACTCCAGGTCACCCACCTGGCTTCAGTCCCCTGCCACCTTACCC 1036
 QY 273 ThrValGlnIeuValThrItpSerTrpGlnLeuProSerArgAlaLeuGlyPro--- 310
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 1064 TGTCCCAACTTGCG-----GCTCCCGAGAGGGTGCACCCCTAT 1108
 QY 311 -----AlaAlaAlaProProLeuSerPro--- 318
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 1109 CACCCGCCACCCGCCACCCGCCACCCGCCACCCGCCACCCGCCACCC 1166
 QY 15 LeuLeuIeuValLeuLeuGlyAlaArgAlaGlyGly----- 26
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 197 CTCCCTGAGCTGTTGGATATAACCCCTCAGGGTTATGGACTGGTCCCCTCACCTA 256
 QY 27 GlyTrpArgSerProArg-----CysAspCysAlaGlyAspPheHisLysSle 43
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 257 GGGGACGSSGAGAGAGATACTGTTGTCGCCAAAGGAAATATGCCCTCACCTA 316
 QY 44 GlyLeuPheCysCysArgGlyCysProAlaGlyHistylLeuLysAlaProCysThrGlu 63
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 317 AATTCGATTCGCTGACCAAGTGGCCACAAGAACCTACTTGTCATCTGTCAGGC 376
 QY 64 ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGlu 83
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 377 CGGGCCAGGATACCGACTGCAAGGGTGTGAGAGGCCCTCTCACCCCTCACAAAC 436
 QY 84 HIS-HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnAla 103
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 437 CACCRCAGA---CACGCTGCAGCTGCTGCTGCAAAAGCAGGAAATATGCCCTCACCTA 316
 QY 104 LeuGluAsnCysSerAlaValAlaLeuAspThrArgCysGlyCysLysProGlyPheVal 123
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 494 ATCTCTCTGTCACAGTGACGCTGCTGCTGCAAAAGCAGGAAATATGCCCTCACCTA 316
 QY 124 GluCys-----GlnValSerGlnCysValSerSerProPheTyrcysGlnInPro 140
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 554 CATATGGCTGAAACCTTTCAGGIC-----TCAATTGAGCC 598
 QY 141 CysteauAspCysGlyValLeuHisArgHisThrArgLeuIeuCysSerTargGasPhe 160
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 599 TGCCCTCAAT---GGACCGTGCAC-----CTCCTCTGCAAGGAGAACAGAAC 643
 QY 161 AspCysGlyIhrCysLeuProGlyPheTrpGluHisGlyAspGlyCysValSerCysPro 180
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 644 ACCGRTGACCTSCCATGCAAGGTTCTTAAGAGAAAACGAGTGTCTCTCTGT--- 700
 QY 181 ThrSerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys----- 195
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 701 -----AGTAACTGTAAGAAGAACCTGGAGTGGCACGAGTGTGCTAACCCAG 748
 QY 196 -----GlyTrpArgGlnMetPheTrpArgValGlnVal 206
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 749 ATTGAGGAATGTTAAGGCCTGAGGACTCTGGCCTGCTGCCCCTGCTCATT 808
 QY 207 LeuAlaGlyLeuIeuValProLeuLeuLeuGlyAlaThrLeuThrThrArgHis 226
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 809 TTCTTGTGTTGTTGCTTATCCCTCTCTCATTTGTTAAATGCTATGCTTACCAAGG 868
 QY 227 CysteProHisLys-----ProLeuValThrAlaAspGluAla 239
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 869 ---TGGAAAGTCCAGCTCTACTCCATGTTGGAAATCGCACCTGAAAGAGGG 925
 QY 240 GlyMetGluAlaLeuThrProProAlaLalaLeuSerProLeuAspSer----- 257
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 926 GAGCTTGAGGACTACTACTAAAGCC-----CTGGCCCAACCCAAGCTTACT 976
 QY 258 -----AlaHistidineLeuAlaProProAspSerSerGluLysileys 272
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 977 CCCACTCCAGGTCACCCACCTGGCTTCAGTCCCCTGCCACCTTACCC 1036
 QY 273 ThrValGlnIeuValThrItpSerTrpGlnLeuProSerArgAlaLeuGlyPro--- 310
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 1064 TGTCCCAACTTGCG-----GCTCCCGAGAGGGTGCACCCCTAT 1108
 QY 311 -----AlaAlaAlaProProLeuSerPro--- 318
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 1109 CACCCGCCACCCGCCACCCGCCACCCGCCACCCGCCACCCGCCACCC 1166
 QY 15 LeuLeuIeuValLeuLeuGlyAlaArgAlaGlyGly----- 26
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 197 CTCCCTGAGCTGTTGGATATAACCCCTCAGGGTTATGGACTGGTCCCCTCACCTA 256
 QY 27 GlyTrpArgSerProArg-----CysAspCysAlaGlyAspPheHisLysSle 43
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 257 GGGGACGSSGAGAGAGATACTGTTGTCGCCAAAGGAAATATGCCCTCACCTA 316
 QY 44 GlyLeuPheCysCysArgGlyCysProAlaGlyHistylLeuLysAlaProCysThrGlu 63
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 317 AATTCGATTCGCTGACCAAGTGGCCACAAGAACCTACTTGTCATCTGTCAGGC 376
 QY 64 ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGlu 83
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 377 CGGGCCAGGATACCGACTGCAAGGGTGTGAGAGGCCCTCTCACCCCTCACAAAC 436
 QY 84 HIS-HisAsnSerGluCysAlaArgCysGlnAlaCysAspGluGlnAlaSerGlnAla 103
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 437 CACCRCAGA---CACGCTGCAGCTGCTGCTGCAAAAGCAGGAAATATGCCCTCACCTA 316
 QY 104 LeuGluAsnCysSerAlaValAlaLeuAspThrArgCysGlyCysLysProGlyPheVal 123
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 494 ATCTCTCTGTCACAGTGACGCTGCTGCTGCAAAAGCAGGAAATATGCCCTCACCTA 316
 QY 124 GluCys-----GlnValSerGlnCysValSerSerProPheTyrcysGlnInPro 140
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 554 CATATGGCTGAAACCTTTCAGGIC-----TCAATTGAGCC 598
 QY 141 CysteauAspCysGlyValLeuHisArgHisThrArgLeuIeuCysSerTargGasPhe 160
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 599 TGCCCTCAAT---GGACCGTGCAC-----CTCCTCTGCAAGGAGAACAGAAC 643
 QY 161 AspCysGlyIhrCysLeuProGlyPheTrpGluHisGlyAspGlyCysValSerCysPro 180
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 644 ACCGRTGACCTSCCATGCAAGGTTCTTAAGAGAAAACGAGTGTCTCTCTGT--- 700
 QY 181 ThrSerThrLeuGlySerCysProGlu-----ArgCysAlaAlaValCys----- 195
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 701 -----AGTAACTGTAAGAAGAACCTGGAGTGGCACGAGTGTGCTAACCCAG 748
 QY 196 -----GlyTrpArgGlnMetPheTrpArgValGlnVal 206
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 749 ATTGAGGAATGTTAAGGCCTGAGGACTCTGGCCTGCTGCCCCTGCTCATT 808
 QY 207 LeuAlaGlyLeuIeuValProLeuLeuLeuGlyAlaThrLeuThrThrArgHis 226
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 809 TTCTTGTGTTGTTGCTTATCCCTCTCTCATTTGTTAAATGCTATGCTTACCAAGG 868
 QY 227 CysteProHisLys-----ProLeuValThrAlaAspGluAla 239
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 869 ---TGGAAAGTCCAGCTCTACTCCATGTTGGAAATCGCACCTGAAAGAGGG 925
 QY 240 GlyMetGluAlaLeuThrProProAlaLalaLeuSerProLeuAspSer----- 257
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 926 GAGCTTGAGGACTACTACTAAAGCC-----CTGGCCCAACCCAAGCTTACT 976
 QY 258 -----AlaHistidineLeuAlaProProAspSerSerGluLysileys 272
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 977 CCCACTCCAGGTCACCCACCTGGCTTCAGTCCCCTGCCACCTTACCC 1036
 QY 273 ThrValGlnIeuValThrItpSerTrpGlnLeuProSerArgAlaLeuGlyPro--- 310
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 1064 TGTCCCAACTTGCG-----GCTCCCGAGAGGGTGCACCCCTAT 1108
 QY 311 -----AlaAlaAlaProProLeuSerPro--- 318
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
 Db 1109 CACCCGCCACCCGCCACCCGCCACCCGCCACCCGCCACCCGCCACCC 1166

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QY 319 -----GluserProLaglySerProAlaMetMethLeuGlnProGlyProGln--- 334
 QY ||||| :
 QY 1169 CAGAACTGGAGCACAGTCACAGGCCACAGGCCACAGGCACACTGATGACCCCGGACG 1228
 QY 335 LeutYrasPvalMetAspAlaValProAlaArgArgPlylspuLeuValArgThrIeu 354
 QY ||||| :
 Db 1229 CTGTAACGCCGGGGAGAACGAGCCCCCGTGGCTGGCTGGAGAAGGATAGCTGGGGCCCTA 1288

QY 355 GlyLeuAaGluAlaGluLleIguLalayallGluValGluLleGlyArg---pheArgAsp 373
 QY ||||| :
 Db 1289 GGCGCTGACCGACCAAGAGATGAGATGGCTGGCTGGAGCTGAGACAGGGCCTGCCCTGGCG 1348

QY 374 GluGlnTrpGluMetLeuIysArgTrpArgGlnGlnGlnPro-----AlaGlyIeu 390
 QY ||||| :
 Db 1349 GCGCAATACAGCCTGCGACCTGGGACGAGGCGACGCGCAGGCGACGCTG 1408

QY 391 GlyAlaValYrrAlaLalaGluGluArgMetGlyIeuAspIyCysValGluAspLeuIeu 410
 QY ||||| :
 Db 1409 GAGCTGCTGGGACGCCGCTCCGCGACATGACCCTGCTGGCTGCCTGGAGACATCGAG 1468

QY 411 SerArgIeu 413
 QY ||||| 1469 GAGGCCTT 1477

RESULT 12

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Sequence 24, Application US/08465982

Patent No. 5863786

GENERAL INFORMATION:

APPLICANT: M. Feldmann, P. W. Gray, M.J.C. Turner, F.M. Brennan

TITLE OF INVENTION: Modified human TNFalpha (Tumor Necrosis Factor alpha) Receptor

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Reed & Robins

STREET: 635 Bryant Street

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,982

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/050,319

FILING DATE: 10-May-1993

ATTORNEY/AGENT INFORMATION:

NAME: Robbins, Roberta L.

REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 5150-0030

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 617-8999

TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 2062 base Pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

FEATURE:

NAME/KEY: CDS

LOCATION: 155..1519

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Alignment Scores:

Score:	Length:	Matches:	Conservative:
Percent Similarity: 39.0%	2062	131	50
Best Local Similarity: 28.29%		182	Mismatches: 182
Query Match: 16.19%		100	Indels: 100
DB: 2		22	Gaps: 22

US-09-993-234-6 (1-417) x US-08-465-982-24 (1-2062)

QY 15 LeutLeuLeuValLeuLeuLleIguLalArgAlaGlyNly----- 26
 QY ||||| :
 Db 197 CTCCUGGAGACCTGTGTTGGGAATAATACCCCTCAGGGGTATTGGACTGGTCCCACCTA 256

QY 27 GlyThrArgSerProArg-----CysAspPysAlaGlyAspPheHisLyslysile 43
 QY ||||| :
 Db 257 GGGGACAGGGAGAGAGATACTGCTGTTGRCCTGGCCAGGAAATAATATCCACCTGAAAT 316

QY 44 GlyLeuPheCysCysArgGlyCysProAlaGlyHisTyruIysAlaProCysThrGlu 63
 QY ||||| :
 Db 317 ATTCGATTTCCTGTTACCAAGTGCCACAAGGAACCTACTTGTCATGACTGTCAGGC 376

QY 64 ProCysGlyAsnSerThrCysLeuValCysProGlnAspThrPheLeuAlaTrpGluasn 83
 QY ||||| :
 Db 377 CGGGGCAGGAATACGACTGCAAGGGAGTGTGAGAGGGCCTCTCACCGCTCAGAAAC 436

QY 84 HisHisAsnSerGluCysAlaArgCysGlnAlaCysAspPgluGlnIaserginValAla 103
 QY ||||| :
 Db 437 CACCTCAGA--CACRCCCTGCTCCTCCAAATGCCAATGGGAATGGGTCAGGTGAG 493

QY 104 LeuGluLysCysSerAlaValAlaAspThrArgCysGlyCysLysProGlyIrpPheVal 123
 QY ||||| :
 Db 494 ATCTCTCTGACAGRCGACCCGGGACACCGGCTGCTGGCTGGAGAGAACAGTAGCGG 553

QY 124 GLUCYS-----GlnValSerGlyCysValSerSerSerProPheThrTyrCysGlnPro 140
 QY ||||| :
 Db 554 CATTATGGAGTGTGAAACCTTTCAGTCAGC 598

QY 141 CysLeuAspCysGlyAlaLeuHisArgLisThrArgLeuLeuCysSerArgGlyAspThr 160
 QY ||||| :
 Db 599 TGCCTCAAT--GGGACCGTGCAC-----CAGCAGGAAACAGAC 643

QY 161 AspCysGlyThrCysLeuProGlyPheThrArgLysGlyIysAspGlyCysValSerCysPro 180
 QY ||||| :
 Db 644 ACCGGTGTGCACCTGCATGGAGGITCTTCTAAAGAGAAACGGAGTGTCTCTCTGT--- 700

QY 181 ThrSerThrIeuGlySerCysProGlu-----ArgCysAlaAlaValCys----- 195
 QY ||||| :
 Db 701 -----ASPARTGCTGAAAGAAAGCTGGGTGCAAGAAGTGTGCTTACCCAG 748

QY 196 -----GlyTrpArgGlnMetPheTrpPheTrpValGluValLeu 206
 QY ||||| :
 Db 749 ATTGAGAATGTTAACGGCACTGAGGACTCGAGCACACAGCAGCTGCTGCTGCCCTGGCATT 808

QY 207 LeuAlaGlyLeuValValProLeuLeuLleIguLalThrIeuThrThrThrThrArgIeu 226
 QY ||||| :
 Db 809 TTCTTGTCTTGTGCCCTTATCCCTCCTCTCATGGTTAATSTATGCTTACCAACGG 868

QY 227 CystTrpProHisLys-----ProLeuValThrAlaAspGluAla 239
 QY ||||| :
 Db 869 --TGGAACTGCAAGGCTACTCCATGTTGTTGGAAATCGACACTGAAAGAGGG 925

QY 258 -----AlaHistIeuLeuAlaProProAspSerSerGluLysIleCys 272
 QY ||||| :
 Db 977 CCCACTCCAGGCTCACCCCCACCTGGCTCAAGCTCCACCTTCACCA 1036

QY 273 ThrValGlnLeuValGlyAsnSerThrProGlyIyrProGluIurGlnGluAlaLeu 292
 QY ||||| :
 Db 1037 TCC-----AGCTCCACCTAACCCCGGTGAC----- 1063